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RESEARCH ARTICLE

Genetic analysis of groundnut (*Arachis hypogaea* L.) genotypes for yield and oil quality parameters

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Abstract

Genetic variability is a foundation for advancing crop improvement programs. The effectiveness of selection is influenced by the characteristics, scope and degree of genetic variability found in the material, as well as the extent to which this variability is heritable. This study assessed fifteen traits, including yield and oil quality parameters, in 55 groundnut accessions from diverse origins. The analysis of genetic parameters, including phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genetic advance as a percentage of the mean (GAM), skewness and kurtosis revealed significant genetic variation for several key traits. Notably, the traits *viz.,* the number of branches (NB)/plant, hundred pod weight, shelling percentage (SP), oil yield/plant and oleic acid (OA) content exhibited high PCV, GCV, heritability and GAM. The analysis showed significant genetic variability and a predominance of additive gene effects, suggesting phenotypic selection as an effective approach for groundnut improvement. Association analysis revealed positive genotypic and phenotypic correlations of single plant yield (SPY) with traits like days to first flowering (DFiF), NB per plant, number of pods (NP) per plant, hundred pod weight, oil yield per plant (OYPP) and OA content. Principal component analysis (PCA) identified five principal components with eigenvalues greater than 1, explaining 75.13% of the total variation. A biplot constructed using the first two PCs visually represented the importance of NP/plant, NB/plant, oil yield/plant and OA content for yield improvement strategies. Cluster analysis efficiently grouped the 55 genotypes into five distinct clusters. The high OA lines "Girnar 4" and "Girnar 5" were clustered together. This information suggests that selecting accessions from clusters with greater genetic distance can be a valuable strategy to maximize genetic variability within breeding programs.

Keywords

correlation; cluster analysis; PCA; groundnut; variability

Introduction

Arachis hypogaea L., recognized as the peanut, is a leguminous crop native to South America. This oilseed and food crop possesses significant genetic diversity, crucial to global food security. Groundnut, being a tetraploid species (2n = 4x = 40), presents unique genetic analysis and breeding challenges due to its duplicated chromosomal complement. The tetraploid cultivated species of groundnut, with an AABB genome, originated from a single hybridization event between two diploid species, followed by chromosome doubling. This unique origin has resulted in relatively low genetic variability. The polyploid nature of

groundnuts has posed significant challenges to their genetic improvement. Many economically important traits, such as yield and oil quality, are polygenic, further complicating the breeding process. Conducting genetic variability studies using robust statistical methods is crucial for uncovering unexploited variation. Such efforts will facilitate the selection of superior breeding material for effective use in hybridization programs (1). Belonging to the Fabaceae family, it is renowned for its high oil content(OC) (45-55%), protein-rich kernels (20-30%), nitrogen-fixing capabilities and promoting soil fertility. Globally, India and China are the leading producers of groundnut cultivation, contributing to over half of the world's total production. Groundnut productivity, on average, ranges from 1.5 to 2.0 metric tons per hectare globally (2). India holds the top position in cultivated areas and ranks second in production. Andhra Pradesh and Gujarat account for approximately 50% of the total groundnut production in India.

Meanwhile, Tamil Nadu and Karnataka have experienced a consistent rise in their production levels over the years (3). Groundnut exhibits remarkable genetic variability, encompassing diverse traits, including pod size, oil content, disease resistance and drought tolerance. However, it may possess a constricted genetic base as a self-pollinated crop. Identifying and leveraging genetic diversity is crucial for crop enhancement and the development of effective selection strategies. Genetic enhancement in any crop primarily relies on the effective use of variability and the implementation of suitable breeding methods is essential. The evaluation of genetic variability and the extent of the transmission of favorable traits are essential for developing an effective breeding program. Hence, it is necessary to evaluate variability and the type of association among economically important characters and partition the overall variability into heritable and non-heritable components for effective selection (4). Broad-sense heritability and genetic gain expressed as a percentage of the mean serve as valuable biometric instruments for plant breeders, aiding in assessing the extent and orientation of selection. Principal component analysis for yield and yield attributes is a statistical method to investigate genotype variability. This technique effectively reduces the dimensionality of a dataset containing numerous measurements to a limited number of principal components that capture the primary patterns. The present study evaluates the variability, character associations, principal component analysis and clustering patterns for yield and its constituent traits. The main objective of this research is to hold significant value in harnessing the existing variability within these traits and choosing superior genotypes grounded in yield outcomes and related characteristics.

Materials and Methods

The current study consisted of 55 groundnut accessions, which included varieties and advanced breeding cultures. The list of groundnut accessions utilized in the current study is given in Table 1. During *Kharif* 2023, the genotypes were planted in a Randomized Block Design at the Department of Oilseeds, CPBG, TNAU, Coimbatore. Two replications of the genotypes were raised and planting was done with 30 cm row spacing and 20 cm between individual plants. The total plot size is 0.3 m^2. The crop cultivation practices recommended for groundnuts were given promptly to facilitate good crop growth. Five competitive plants for all the genotypes from the two replications were chosen to record the biometrical observations. The following observations such as DFiF, Days to 50% flowering (DFF), Plant height (PH-cm), NB per plant, NP per plant, Hundred pod weight (HPW), Hundred kernel weight (HKW-g), Shelling percent (SP), Single plant yield (SPY), OC, OYPP and Fatty acid content such as OA, Linoleic acid (LA), Stearic acid (SA) and Palmitic acid (PA) were recorded. The OC and fatty acid composition were estimated using Near-Infrared Spectroscopy (Make: M/s ZEUTEC, Germany; Model: SPA 1.0) calibrated with a standard library based on reference values.

Statistical analyses

The collected data were subjected to analysis of variance in a randomized block design using TNAU STAT. Variability parameters such as PCV and GCV were estimated to partition total variation into genetic and environmental components, as these parameters are widely used to assess variability in polygenic traits. If the PCV and GCV value is less than 10 %, it is low, if the value is between 10 -20 %, it is moderate, if the value is more than 20 %, it is considered high (5). Broad sense heritability (6, 7) and genetic advance (8) were calculated to evaluate the potential for improvement through selection. The heritability is classified (9) as low (<30 %), medium (30 - 60%) and high (>60%). Similarly, the genetic advance as a percent of the mean is also classified as low (<10%), medium (10-20%) and high (>20%). The skewness and kurtosis were estimated to evaluate the dataset's distribution and symmetry (10). The association analyses, such as Principal component analysis (PCA) were employed to identify major contributors to trait variability (11) and hierarchical clustering grouped genotypes based on their similarity. The variability parameters, PCA and clustering were done in R software version 4.4.1 with the package *metan* for variability, *FactoMineR* for PCA and *dendextend* for clustering.

Results

In the ANOVA analysis, the significant p-value indicates statistically significant differences between the genotypes, demonstrating sufficient variability in the material studied. Significant variations were present among the genotypes across all characteristics (Table 2). The trait HPW showed significant variability with the high mean sum of square value of 1710.360** (Table 2), ranging from 66.13 g to 180.93 g. The coefficient of variation ranged from 6.66% for days to fifty percent flowering to 37.60% for the trait OYPP. The traits DFiF, DFF and OC showed low CV and PH, LA, PA, SA showed moderate CV. High CV was observed for NB, NP, HPW, HKW, SP, OA and SPY traits. The highest CV for the trait OYPP suggests greater variability (Table 3).

Table 1. List groundnut genotypes used in the present study

S.No	Genotypes	Source	Type
1	ALR1	CRS, Aliyarnagar	Semi-spreading
2	ALR2	CRS, Aliyarnagar	Bunch
3	ALR3	CRS, Aliyarnagar	Bunch
4	BSR2	ARS, Bhavanisagar	Bunch
5	CO1	Dept. of Oilseeds, Coimbatore	Bunch
6	CO2	Dept. of Oilseeds, Coimbatore	Bunch
7	CO3	Dept. of Oilseeds, Coimbatore	Bunch
8	CO4	Dept. of Oilseeds, Coimbatore	Bunch
9	CO5	Dept. of Oilseeds, Coimbatore	Semi-spreading
10	CO6	Dept. of Oilseeds, Coimbatore	Semi-spreading
11	CO7	Dept. of Oilseeds, Coimbatore	Bunch
12	TMV1	ORS, Thindivanum	Bunch
13	TMV2	ORS, Thindivanum	Bunch
14	TMV7	ORS, Thindivanum	Bunch
15	TMV10	ORS, Thindivanum	Semi-spreading
16	TMV13	ORS, Thindivanum	Bunch
17	TMV14	ORS, Thindivanum	Bunch
18	VRI2	RRS, Vridhachalam	Bunch
19	VRI3	RRS, Vridhachalam	Bunch
20	VRI4	RRS, Vridhachalam	Bunch
21	VRI5	RRS, Vridhachalam	Bunch
22	VRI6	RRS, Vridhachalam	Bunch
23	VRI7	RRS, Vridhachalam	Semi-spreading
24	VRI8	RRS, Vridhachalam	Bunch
25	VRI9	RRS, Vridhachalam	Bunch
26	VRI10	RRS, Vridhachalam	Bunch
27	GG20	ICAR-Directorate of Groundnut Research,Junagadh, Gujarat	Semi-spreading
28	GG33	ICAR-Directorate of Groundnut Research, Junagadh, Gujarat	Semi-spreading
29	GG7	ICAR-Directorate of Groundnut Research, Junagadh, Gujarat	Bunch
30	K6	Kadiri, ANGARU, Andhra Pradesh	Bunch
31	K9	Kadiri, ANGARU, Andhra Pradesh	Bunch
32	DHARANI	RARS, Tirupati, Andhra Pradesh	Bunch
33	TAG24	BARC, Trombay	Semi-spreading
34	TG37A	BARC, Trombay	Bunch
35	GPBD4	UAS, Dharwad	Bunch
36	JL24	Oilseeds Research Station, Jalgaon, Maharashtra	Bunch
37	WESTERN44	Western Agri Seeds Ltd., Gujarat	Semi-spreading
38	ASHA	ICRISAT, Hyderabad	Semi-spreading
39	AK303	Akola, Maharashtra	Bunch
40	GANGAPURI	Madhya Pradesh	Bunch
41	R2001/2	UAS, Raichur	Bunch
42	COG0537	TNAU, Coimbatore	Bunch
43	COG0539	TNAU, Coimbatore	Bunch
44	COG0549	TNAU, Coimbatore	Bunch
45	CHICO	An early-maturing germplasm line from USA	Bunch
46	COG17007	Dept. of Oilseeds, CPBG, TNAU, Coimbatore	Bunch
47	GIRNAR4	ICAR-Directorate of Groundnut Research, Junagadh, Gujarat	Bunch
48	GIRNAR5	ICAR-Directorate of Groundnut Research, Junagadh, Gujarat	Bunch
49	COG17007	Dept. of Oilseeds, Coimbatore	Bunch
50	COG20-04	Dept. of Oilseeds, Coimbatore	Bunch
51	COG20-12	Dept. of Oilseeds, Coimbatore	Bunch
52	COG22-04	Dept. of Oilseeds, Coimbatore	Bunch
53	COG18-37	Dept. of Oilseeds, Coimbatore	Bunch
54	COG17006	Dept. of Oilseeds, Coimbatore	Bunch
55	COG0543	Dept. of Oilseeds, Coimbatore	Bunch

Table 2. ANOVA for the component traits in fifty-five groundnut genotypes

Characters	Mean sum squares	
	Treatment (df = 54)	Error (df = 108)
DFiF	24.389**	3.628
DFF	24.567**	4.918
PH (cm)	77.348**	25.617
NB	14.968**	2.549
Number of pods per plant	45.527**	12.543
HPW (g)	1710.360**	160.060
HKW (g)	192.914**	8.409
SP (%)	962.961**	125.382
SPY (g)	27.489**	7.568
OC (%)	40.850**	3.226
OYPP (g)	500.890**	500.890
LA (%)	99.504**	1.043
OA (%)	203.952**	1.128
PA (%)	11.873**	0.211
SA (%)	1.250**	0.008

Phenotypic and genotypic coefficient of variation

The estimates of genetic variability parameters are represented in Table 3. High GCV was observed for traits such as NB, NP, HPW, SP, SPY, OYPP and OA. Moderate GCV for traits such as PH, HKW, LA, PA and SA. The high PCV was found for traits such as PH, NB, NP, HPW, HKW, SP, SPY, OYPP and OA. Moderate PCV was observed for traits such as LA, PA and SA. The low GCV and PCV were observed for traits such as DFiF, DFF and OC. Combining both, the traits NB, NP, HPW, SP%, OYPP, OA and SPY showed high GCV and PCV. The traits LA, PA and SA showed moderate GCV and PCV. Moderate GCV and high PCV were observed for PH and HKW traits (Table 3).

Heritability and genetic advance as percent of mean

High broad-sense heritability was observed for characters such as DFiF, NB, HPW, HKW, SP, OC, OYPP, OA, LA, PA and SA, suggesting that additive genetic factors largely influence these traits. The traits NB, NP, HPW, HKW, SP%, OYPP, LA, OA, PA, SA and SPY showed high GAM. The traits NB, HPW, HKW, SP, OYPP, LA, OA, PA and SA had high GAM and heritability (Table 3).

Skewness and kurtosis

Negative skewness was observed for the traits DFiF, LA and PA, indicating that most genotypes have higher values for these traits. Positive skewness was observed for the traits NB, NP, HPW, HKW, OYPP, OA content and SPY, which denotes that most genotypes have lower values for these traits. The traits such as DFiF, PH, NP, HKW, OC, OYPP, LA, OA and SPY had a leptokurtic distribution in which most data points are concentrated around the mean with fewer extremes. DFF, NB and SP traits had a platykurtic curve, representing a more uniform distribution with fewer extremes. (Table 3) The violin plot for the 15 traits in Fig. 1. shows the distribution of the dataset.

Association studies

Correlation studies: The genotypic and phenotypic correlation coefficient for yield and its component traits are given in Table 4. When considering the SPY, almost all the traits except the traits *viz.,* DFF, HKW, OC, LA content and SA had significant genotypic correlation with SPY. The traits DFiF, NB, NP, HPW, OYPP and OA had a significant positive genotypic correlation with SPY. A significant negative genotypic correlation with SPY was observed for PH, SP and PA content traits.

Phenotypic Correlation

measures the correlation between observed traits and includes both G + E (genetic and environmental) effects. A significant and positive phenotypic correlation was observed between the traits viz., NB, NP, HPW, HKW, OYPP, OA content

Table 3. Estimation of genetic parameters for biometrical traits

S.No.	Characters	Mean	CV %	Range		GCV %	PCV %	Heritability (bs) (h^2)	GA as % of mean	Skewness	Kurtosis
				Min.	Max.						
1	DFiF	34.99	8.15	27.00 (TMV 2)	40.67 (GG33)	7.52	9.28	65.60	12.54	-0.692*	0.621*
2	DFF	42.99	6.66	36.67 (CO4)	49.00 (ASHA)	5.95	7.88	57.11	9.27	-0.542	-0.044*
3	PH (cm)	31.92	15.91	18.67 (COG22-04)	45.33 (CO4)	13.01	20.51	40.23	17.00	0.301	0.542*
4	NB	7.09	31.51	4.33 (VRI 10)	12.00 (CO5)	28.69	36.47	61.88	46.50	0.733*	-0.873*
5	NP	13.57	28.71	9.00 (CO6)	29.33 (COG20-04)	24.44	35.75	46.71	34.40	2.285*	6.200*
6	HPW (g)	95.46	25.01	66.13 (VRI5)	180.93 (AK303)	23.81	27.25	76.35	42.87	1.457*	2.550
7	HKW (g)	39.44	20.33	25.43 (CO1)	64.61 (AK303)	19.88	21.20	87.97	38.42	1.196*	1.395*
8	SP (%)	54.45	27.03	23.07 (CO1)	86.25 (VRI7)	26.99	27.12	99.01	55.33	0.493	-0.414*
9	OC (%)	47.16	7.82	36.66 (TMV13)	54.59 (CO2)	7.51	8.42	79.54	13.80	0.016	0.077*
10	OYPP (g)	32.85	37.60	10.24 (TMV10)	71.22 (COG20-04)	37.56	37.67	99.10	77.16	0.996*	1.159*
11	LA (%)	42.69	17.73	5.98 (GIRNAR5)	54.36 (VRI4)	13.26	13.46	98.38	26.88	-2.673*	10.673*
12	OA (%)	40.08	20.57	26.42 (VRI4)	79.42 (GIRNAR5)	20.52	20.69	98.46	41.92	2.269*	9.326*
13	PA (%)	17.83	11.15	9.79 (GIRNAR4)	21.48 (VRI4)	11.06	11.35	94.48	22.18	-1.153*	3.737
14	SA (%)	3.77	17.09	1.67 (VRI10)	5.66 (ALR1)	17.05	17.23	99.51	34.76	0.228	2.377
15	SPY (g)	10.86	27.86	4.80 (VRI7)	21.29 (COG20-04)	23.72	34.70	46.73	33.40	0.999*	1.508*

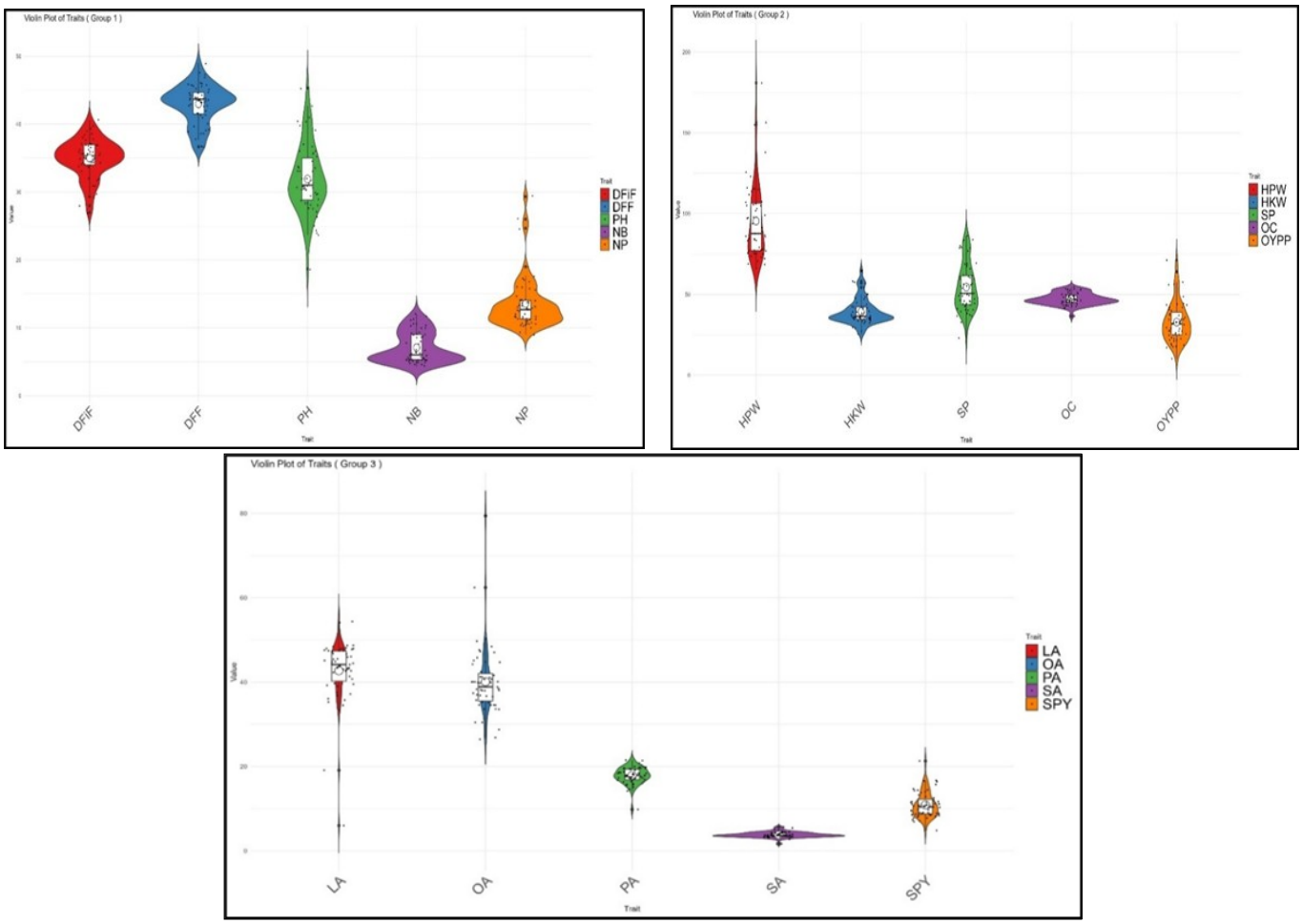

Fig. 1. Violin plot showing the data distribution for the yield and oil quality traits. Days to first flowering (DFiF), Days to 50% flowering (DFF), Plant height (PH), Number of branches per plant (NB), Number of pods per plant (NP), Hundred pod weight (HPW), Hundred kernel weight (HKW), Shelling percent (SP), Single plant yield (SPY), Oil content (OC), Oil yield per plant (OYPP) Oleic acid (OA), Linoleic acid (LA), Stearic acid (SA) and Palmitic acid (PA).

Table 4. Correlation coefficients among component traits of fifty-five groundnut genotypes

Character	DFiF	DFF	PH	NB	NP	HPW	HKW	SP	OC	OYPP	LA	OA	PA	SA	SPY
DFiF	1	1.0087**	-0.3942**	0.0886	0.295*	0.1099	0.2031	0.2333	-0.076	0.3581**	-0.1231	0.2056	-0.3697**	-0.1013	0.3081*
DFF	0.6039**	1	-0.4799**	0.1163	0.0523	0.2223	0.3603**	0.2466	-0.1251	0.2556	-0.109	0.1227	-0.2325	-0.0176	0.1865
PH	-0.1896*	-0.2754**	1	-0.5612**	-0.3399*	-0.0778	-0.0258	-0.1423	0.1994	-0.2889*	0.1128	-0.2093	0.3963**	-0.0749	-0.3096*
NB	0.0661	0.1046	-0.2625**	1	0.6482**	-0.2574	-0.3267*	0.1058	0.1526	0.3795**	-0.356**	0.4135**	-0.4458**	-0.0502	0.2707*
NP	0.1122	-0.0047	-0.1947*	0.3668**	1	-0.1383	-0.4318**	0.1793	0.2493	0.8906**	-0.314*	0.5385**	-0.6071**	-0.1056	0.5545**
HPW	0.0545	0.095	-0.038	-0.1957*	-0.0291	1	0.7004**	-0.2986*	-0.131	0.3376*	0.0116	0.031	0.1104	0.0193	0.6449**
HKW	0.187*	0.2385**	0.0092	-0.2063**	-0.196*	0.5837**	1	0.2007	-0.1838	0.2808*	0.0923	-0.0677	-0.005	-0.1632	0.2359
SP	0.1896*	0.1875*	-0.0839	0.0831	0.1157	-0.2574**	0.1925*	1	-0.085	0.2585	0.0325	0.0437	-0.1255	-0.2373	-0.3695**
OC	-0.0661	-0.0818	0.1884*	0.0686	0.1075	-0.1441	-0.1419	-0.0759	1	0.347**	-0.2127	0.1626	-0.165	-0.0385	0.1309
OYPP	0.2955**	0.191*	-0.1752*	0.3021**	0.6123**	0.2914**	0.2632**	0.2559**	0.3079**	1	-0.1939	0.4061**	-0.4999**	-0.1526	0.9137**
LA	-0.0755	-0.0706	0.0911	-0.2937**	-0.1992*	0.0254	0.0848	0.0317	-0.1913*	-0.1909*	1	-0.8178**	0.5672**	-0.1178	-0.1576
OA	0.1617*	0.102	-0.133	0.3289**	0.3571**	0.0225	-0.0607	0.0417	0.1505	0.4024**	-0.7959**	1	-0.5455**	-0.0887	0.3574**
PA	-0.2892**	-0.1555*	0.2229**	-0.3269**	-0.3869**	-0.0042	0.0044	-0.1228	-0.145	-0.4851**	0.5405**	-0.5261**	1	0.1428	-0.4754**
SA	-0.0834	-0.0163	-0.038	-0.0395	-0.076	0.013	-0.1565*	-0.2334**	-0.0297	-0.1501	-0.1142	-0.0889	0.1365	1	0.0114
SPY	0.1337	0.0722	-0.1455	0.1785*	0.7112**	0.4359**	0.2501**	-0.251**	0.0278	0.6275**	-0.0937	0.2332**	-0.3065**	-0.0018	1

Significant at 5% = * and significant at 1%= **, Phenotypic level = down ward left side of diagonal, Genotypic level = upward right side of diagonal

and SPY. The traits like SP and PA have significant negative phenotypic associations with SPY. The correlogram in Fig. 2. shows the phenotypic and genotypic correlation coefficients.

Diversity analysis

Principal Component Analysis (PCA): The PCs with eigenvalue of more than 1, i.e., PC1 (4.2858), PC2 (2.4786), PC3(1.9033), PC4 (1.3630) and PC5(1.2388) contribute maximum to the variability. The principal components with the eigenvectors are given in Table 5. The other principal components with eigenvalue less than 1, *i.e.,* PC6 to PC15, are less explanatory and are thus not retained. The results indicate that the first five PCs explain 75.13% of the total variance. The first PC with an eigenvalue of 4.2858 explained 28.57 % of the total variability. PC1 gave high positive weight for DFiF, DFF, NB, NP, HPW, HKW, SP, SPY, OC, OYPP and OA. The PC1 negatively correlates with PH, LA, PA and SA traits.PC2, with a value of 2.478, contributes 16.52% of the total variability. The PC2 is positively correlated with all other traits except PH, NB, NP, OC, OA content and SA content, which indicates that these traits are not aligned with the variation explained by PC2. The third PC with an eigenvalue of 1.9033 accounted for 12.69% of the total variability, with the traits viz., DFiF, DFF, NB, SP and LA contributing positively towards PC3. The PC4 with an eigenvalue of 1.3630 showed 9.09% of the total variability

Table 5. Principal Component Analysis of five components

Particulars	PC1	PC2	PC3	PC4	PC5
Eigen value	4.2858	2.4786	1.9033	1.3630	1.2388
Variability %	28.57	16.52	12.69	9.09	8.26
Cumulative %	28.57	45.10	57.78	66.87	75.13
Variable	**Eigen vector**				
DFiF	0.2306	0.3096	0.3410	-0.0876	0.1122
DFF	0.1805	0.3693	0.3626	-0.1672	0.1622
PH (cm)	-0.2131	-0.1060	-0.2500	0.4268	0.1842
NB	0.2775	-0.2357	0.1629	-0.1728	-0.2149
Number of pods per plant	0.3810	-0.1827	-0.0403	0.0203	-0.3602
HPW (g)	0.0785	0.4412	-0.4272	-0.0544	0.0854
HKW (g)	0.0271	0.5190	-0.1222	0.2537	0.1685
SP (%)	0.0734	0.0586	0.4716	0.4358	-0.0681
SPY (g)	0.3332	0.1711	-0.3996	-0.1162	-0.2495
OC (%)	0.1075	-0.2278	-0.1726	0.3158	-0.0219
OYPP (g)	0.4042	0.1164	-0.1495	0.2304	-0.2563
LA (%)	-0.3060	0.2530	0.0918	0.0025	-0.5536
OA (%)	0.3508	-0.1862	-0.0455	0.0318	0.5109
PA (%)	-0.3576	0.0541	-0.0658	-0.0365	-0.0609
SA (%)	-0.0627	-0.0625	-0.1229	-0.5704	0.1060

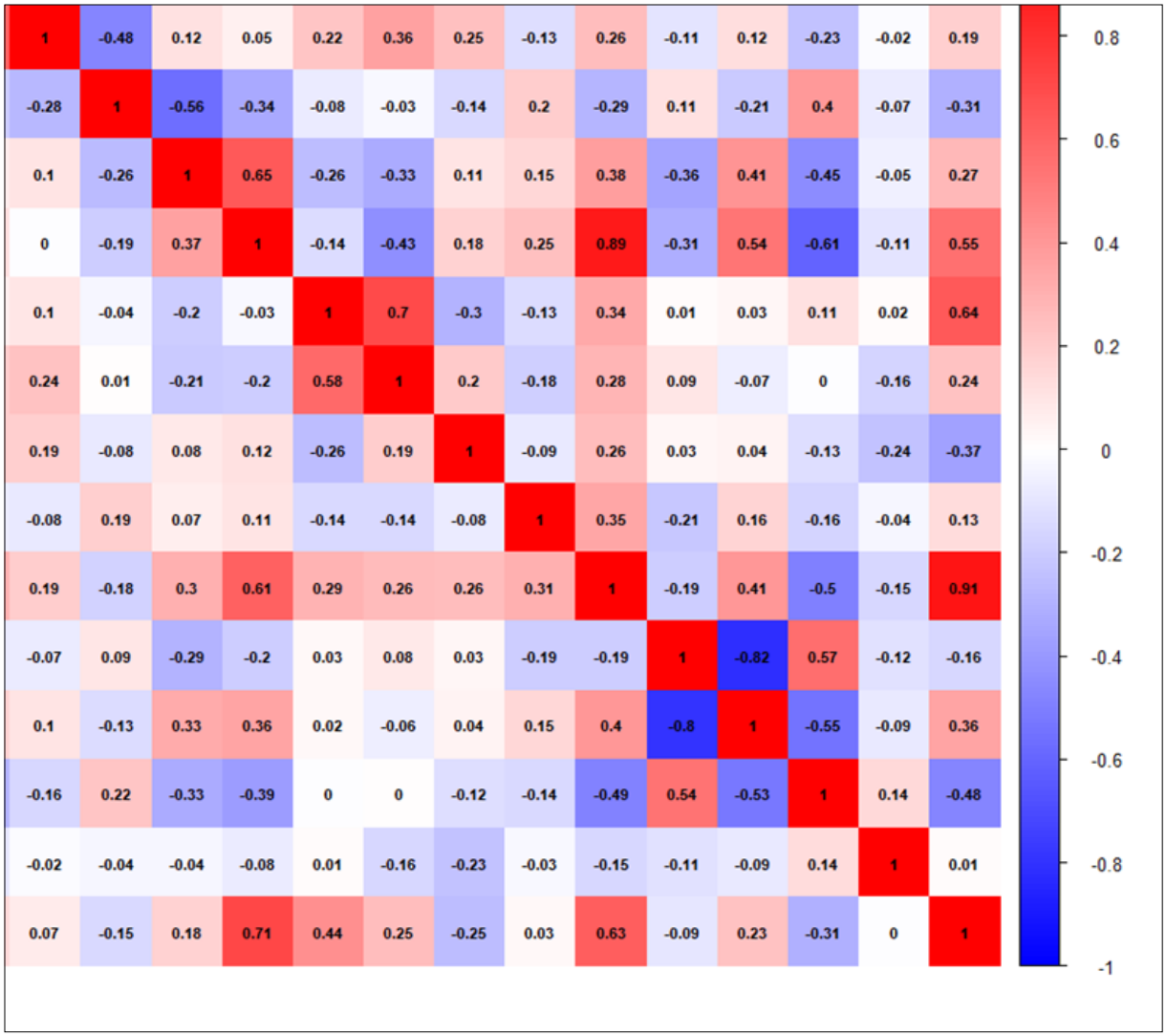

Fig. 2. Correlogram for correlation coefficients among component traits of fifty-five groundnut genotypes.

Phenotypic level = downward left side of diagonal, Genotypic level = upward right side of diagonal.

with the traits PH, NP, HKW, SP, OC, OYPP, LA and OA correlated positively with PC4. About 8.26% of the total variability is accounted for by PC5, with an eigenvalue of 1.2388. The traits, viz., NB, NP, SP, SPY, OC, OYPP, LA and PA, contributed negatively to PC5.

The PCA biplot reveals the relationships among traits based on the angles and orientations of their vectors (Fig. 3). Traits with vectors forming acute angles positively correlate, indicating a strong association. The traits HKW and HPW are positively correlated, as are DFF and DFiF, suggesting they contribute similarly to variability. Similarly, traits such as SA and PH, SPY and OYPP, NP and OA and SP and SPY, exhibit positive correlations due to the alignment and proximity of their vectors. In contrast, traits with vectors forming obtuse angles or pointing in opposite directions are negatively correlated. The trait NP is negatively correlated with HKW and HPW, OA shows a negative relationship with LA and OC is negatively correlated with HKW and HPW. Traits with vectors forming right angles are uncorrelated, indicating no linear relationship. The trait LA is uncorrelated with DFiF and DFF, while OA shows no association with DFiF. Similarly, PA is uncorrelated with HKW and HPW, NP has no correlation with DFiF and OC is not associated with SPY. The traits such as HKW, NP and OYPP have longer vectors, whereas PH, SA and SP have shorter vectors.

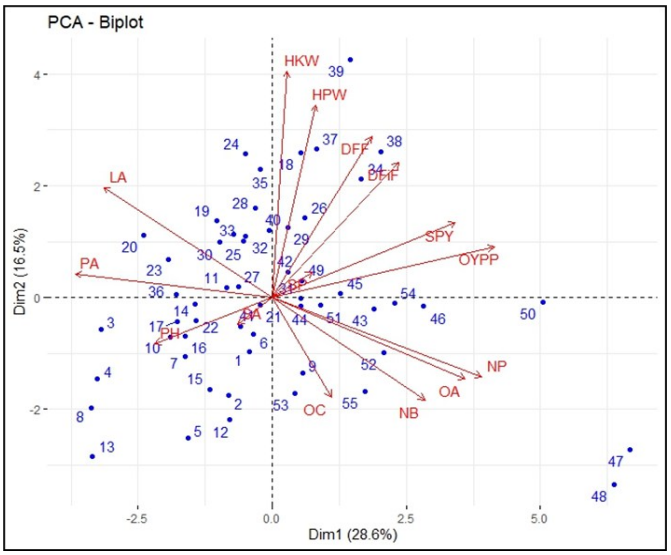

Fig. 3. Genotype by trait biplot showing distribution of genotypes across first two PCs.

Cluster analysis

Cluster analysis was performed using Ward's agglomerative clustering method with Euclidean distance measure for fifty-five groundnut genotypes, which resulted in five clusters. The components of each cluster are detailed in Table 6. Cluster I is the largest cluster, with 21 genotypes constituting 38.18% of the total genotypes, followed by Cluster III with 17 genotypes (30.9%). Cluster II (12.7%), IV (14.5%) and V (3.6%) have 7,8 and 2 genotypes, respectively. The average intra and inter-cluster distances among the ten clusters are presented in Table 7. The maximum intra-cluster distance was observed for Cluster V (0.313), followed by Cluster II (0.258), Cluster IV (0.170), Cluster I (0.0964) and Cluster III (0.038). The maximum inter-cluster distance between clusters II and V was found (8.726). The minimum inter-cluster distance was found between the cluster III and Cluster I (2.645). Combined with a dendrogram (Fig. 4), the heatmap illustrates the hierarchical clustering of 55 groundnut genotypes based on the observed traits.

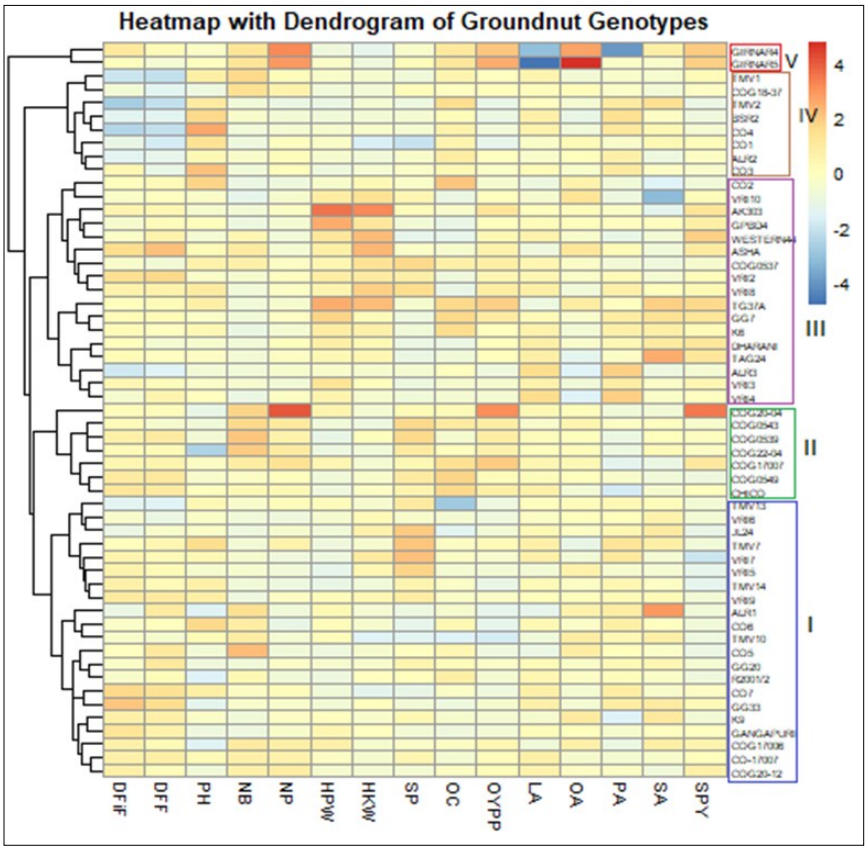

Fig. 4. The heatmap combined hierarchical clustering of 55 groundnut genotypes based on yield and oil quality parameters.

Table 6. Cluster composition of the fifty-five genotypes

Clusters	Number of genotypes	Accessions
I	21 (38.18%)	TMV13, VRI6, JL24, TMV7, VRI7, VRI5, TMV14, VRI9, CO6, TMV10, CO5, GG20, R2001/2, CO7, GG33, K9, GANGAPURI, COG17006, COG17007, COG20-12, ALR1
II	7 (12.7%)	COG20-04, COG0543, COG0539, COG22-04, COGO549, CHICO, COG17007
III	17 (30.9%)	VRI4, VRI3, ALR3, TAG24, DHARANI, K6, GG7, TG37A, VRI8, VRI2, COG0537, ASHA, WESTERN44, GPBD4, AK303, GG20, CO2
IV	8 (14.5%)	CO3, ALR2, CO1, CO4, BSR2, TMV2, TMV1, COG18-37
V	2 (3.6%)	GIRNAR4, GIRNAR5

Table 7. Inter and Intra-cluster distances

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	0.0964	3.385	2.645	3.499	8.139
Cluster II		0.258	3.952	4.989	8.726
Cluster III			0.038	3.950	8.348
Cluster IV				0.170	6.458
Cluster V					0.313

Discussion

selection in these traits. Similar genetic variability studies in groundnut were reported in which low GCV and PCV were observed for the traits DFiF (12-15), DFF (16, 17) and OC (18, 19). The traits LA, PA and SA showed moderate PCV and GCV, which offers moderate selection efficiency as there is reasonable genetic variation present in these traits. Studies related to groundnut's nutritional and oil quality traits, such as LA (20), SA and palmitic acid (21), also showed moderate GCV and PCV values.

High PCV combined with high GCV is observed for the traits NB, NP, HPW, SP%, OYPP, OA and SPY. This represents that most of the yield-related traits grouped here have significant genetic variability and have a high potential for improvement through selection. Studies related to groundnut genetic variability for yield and yield-related traits also reported high estimates of PCV and GCV for NB (16, 22); NP (17, 18); HPW (18); SP % (19); SPY (23); OYPP (16, 17, 24); OA (23). It can be seen that, for all the traits, the difference between the PCV and GCV values is minimal, indicating that the observed phenotypic variability of the trait is due to genetic differences. Selection based on phenotypic performance is likely to be effective since the phenotype accurately reflects the genotype (25).

Heritability and Genetic advance as percent of mean

High broad-sense heritability was observed for DFiF, NB, HPW, HKW, SP, OC, OYPP, OA, LA, PA and SA characters. Similar findings were observed for NB (8), HPW (18, 19, 26); HKW (17, 19, 26) and DFiF (26), where the heritability was high. High heritability, along with high GAM, indicates that a trait is under strong genetic control and significant improvement can be achieved through selection. Conversely, low heritability and GAM suggest that environmental factors play a larger role in trait variation and improvement through selection might be more challenging. The traits NB, HPW, HKW, SP, OYPP, LA, OA, PA and SA had high GAM and heritability. Related findings in which the variability parameters studied in groundnut genotypes for the yield-related traits under diverse environments showed high heritability with high GAM for the traits NB and HKW (27); SA and LA (21); HKW and OA (28). Genetic advances during selection estimate the expected improvement in a trait. When combined with high heritability, the traits have a strong additive genetic component and can show substantial gains per selection cycle. These traits could be utilized in hybridization programs, where elite parents with desirable high heritability traits could be crossed to maximize genetic potential. The traits governing the fatty acid composition are LA, OA, PA and SA, where high heritability leads to the development of varieties with improved oil quality. The traits such as NB, HPW, HKW and SP directly enhance the yield and economic value of the crop.

Association studies

Correlation studies: Yield is a multifaceted trait shaped by various genetic and environmental influences. Direct selection for yield is difficult as it is controlled by many genes and their relation to environmental elements. Therefore, indirect selection methods utilizing correlation among traits to enhance yield are followed for crop improvement. The phenotypic correlation considers genetic and environmental factors, whereas the genotypic correlation, which considers only the genetic level, is stable across environments. Positive correlations among desirable traits can be leveraged to improve multiple traits simultaneously, while negative correlations might require balancing during selection. The results demonstrate that the trait SPY has a positive phenotypic and genotypic correlation with traits such as NB, NP, HPW, OYPP and OA. Parallel research studies for association analysis in groundnut for yield and its component studies also showed a positive genotypic and phenotypic correlation between SPY and NB, NP, HKW (29) and OYPP (30). A significant negative phenotypic and genotypic correlation was observed between SPY and SP, PA. These results were supported by the relevant studies on groundnuts, in which there was a significant negative correlation between SPY and SP (31) and PA (32). Leveraging the traits positively correlated with the SPY will help develop improved varieties with high yields and good oil quality.

Diversity analysis

Principal Component Analysis: The study shows that the first five principal components contribute 75.13 % of the total variability. Relevant studies of multivariate analysis in groundnut were reported in which the first five principal components (PCs) each had an eigenvalue exceeding one, collectively accounting for approximately 71.83 % of the total observed variation (33). It was also concluded that pod weight/ plant traits and the NP contributed to PC1. The PC2 positively influenced OA content, while PC3 was positively associated with days before flowering. NP contributed positively towards PC4. Reports were also found in which the first five principal components, with more than 1, explained about 73.24% of the total variation and the first principal component assigned a high positive weight to HPW and HKW (34).

Based on the results of the biplot analysis, the angle between the vectors shows the relationship between the variables. PCA biplot analyses in groundnut for yield and oil quality traits showed similar results in which HKW and HPW showed a positive correlation (35) between SPY and OYPP (36) and a negative correlation between OA and LA (35). The longer vector length of HKW, NP and OYPP shows that these traits have a greater influence on the variability, whereas the shorter vectors of PH, SA and SP contribute less to the variance.

Cluster analysis

The results show that cluster V has two “Girnar 4 and Girnar 5" genotypes with higher OA content than the others. It can be used as the OA donor in breeding programs for oil quality improvement (37). The selection of cluster II and V genotypes will be useful for further breeding programs as they have maximum inter-cluster distance and consist of diverse genotypes. Similar studies in 15 Bambara groundnut accessions for 14 qualitative and 27 quantitative traits grouped the accessions into five distinct clusters based on the UPGMA hierarchical clustering method (38). It was summarized that the genotypes taken for this study are highly diverse and grouped under different clusters and the heatmap shows the variation pattern of the genotypes for all the traits recorded.

Conclusion

Understanding the variability within a population of interest facilitates the development and design of an optimal genotype. Traits such as the NB, HPW, SP, OYPP and OA content emerged as critical targets for phenotypic selection to enhance yield. Additionally, traits like the NP per plant and hundred kernel weight (HKW) showed positive associations with SPY at phenotypic and genotypic levels, reinforcing their importance in breeding programs. The PCA analysis further identified HKW, HPW, DFiF, DFF and OYPP as major contributors to yield variability, making them ideal traits for targeted selection. Cluster analysis revealed wide genetic diversity among genotypes, suggesting that selecting parents from genetically distant clusters for hybridization could generate novel genetic variability, enhance heterosis and broaden the genetic base. By focusing on these critical traits, breeders can develop superior groundnut varieties that combine high-yield potential with improved oil quality, ensuring adaptability to diverse environments and market demands. Integrating phenotypic selection, PCA and cluster analysis in breeding strategies facilitates the development of high-performing genotypes and ensures the long-term sustainability of groundnut cultivation.

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Authors' contributions

MU and KV collected the germplasm, conducted the trial and recorded observations. SRM analyzed the data in different software. PS and SA corrected the drafted manuscript, finalized DK and assisted in recording various laboratory observations. Hence, all the authors have read and approved the manuscript.

Compliance with ethical standards

Conflict of interest: Authors do not have any conflict of interest to declare.

Ethical issues: None

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